

REMARKS

Claims 1-40 constitute the pending claims in the present application. Applicants respectfully request reconsideration in view of the following remarks. Issues raised by the Examiner will be addressed below in the order they appear in the prior Office Action.

1-4. Applicants note that the previous amendment was entered and considered, and that claims 1-13 and 23-36 are withdrawn as being directed to a non-elected invention. Applicants will cancel such claims upon indication of allowable subject matter.

5. Applicants note that item BX on the previous IDS was not considered. This item will not be resubmitted.

6. Claims 14-22 and 37-40 are rejected under 35 U.S.C. § 101 because the claimed invention allegedly lacks patentable utility. Applicants respectfully traverse this rejection.

Faye et al., WO 99/07836, cited as reference BV in the IDS filed January 29, 2001, discloses nucleotide and amino acid sequences with strong similarity to SEQ ID Nos. 13 and 14. For example, SEQ ID No. 2 of Faye et al. differs from SEQ ID No. 14 of the present application by merely six amino acids, 98% identity (see sequence comparison attached as Exhibit A). On page 8, lines 30-36, Faye et al. state that cells transformed by a plasmid encoding SEQ ID No. 2 (CaCIV1) rescues *S. cerevisiae* cells which lack a functional ScCIV1 gene, a gene essential for cell viability. Accordingly, an agent which blocks the function of CaCIV1 would be expected to exhibit antifungal activity. Applicants asserted that the claimed subject matter was useful for drug screening assays on page 4, lines 5-6, and page 9, lines 11-18, and Faye et al. demonstrate the accuracy of these assertions.

Moreover, Applicants submit that use as a diagnostic tool, despite the Office Action's assertions to the contrary, is a *specific and substantial* utility that was asserted in the present application. The mere fact that other sequences may also be used for this purpose does not contradict this utility, or make it any less specific. For example, many different compounds have been identified – and patented – as antidepressant pharmaceuticals. The mere fact that *one* antidepressant is known does not make subsequent compounds identified as having similar

activity any less useful, nor their utility any less specific, as the arguments recited in the Office Action suggest. Accordingly, the mere fact that other nucleic acids identified and sequenced from *C. albicans* could be used for diagnostic purposes does not undercut the fact that the presently claimed subject matter could also be used to diagnose the presence of *C. albicans* in a patient. Contrary to the statements in the Office Action, it is not true that *any* nucleic acid would have this utility. This utility is dependent on the particular sequence disclosed by Applicants, and random sequences would typically be ineffective for this purpose. This fact demonstrates that the asserted utility is, in fact, specific.

For the reasons set forth above, Applicants submit that the pending claims fully comply with the requirements of 35 U.S.C. § 101. Reconsideration and withdrawal of this rejection is respectfully requested.

With respect to the rejection of these claims as not being enabled because the claimed invention was not allegedly supported by a utility, Applicants submit that the uses described above were described in the application with sufficient detail and clarity that one of skill in the art could have practiced the claimed invention throughout its scope. Reconsideration and withdrawal of this rejection is respectfully requested.

7. Claims 37-40 are rejected under 35 U.S.C. §112, first paragraph, as allegedly containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention. Applicants respectfully traverse this rejection to the extent it is maintained over the claims as amended.

Applicants have amended claim 37 to more particularly point out conditions recited on page 13 of the application. Reconsideration and withdrawal of this rejection is respectfully requested.

8. Claims 37-40 are rejected under 35 U.S.C. §112, second paragraph, as allegedly being indefinite. Applicants respectfully traverse this rejection to the extent it is maintained over the claims as amended.

Applicants have amended claim 37 as pointed out above. Applicants submit that hybridization is a common laboratory technique, and that one of skill in the art would readily be able to determine whether or not a nucleic acid sequence hybridizes to another under specified conditions. Reconsideration and withdrawal of this rejection is respectfully requested.

CONCLUSION

In view of the foregoing amendments and remarks, Applicants submit that the pending claims are in condition for allowance. Early and favorable reconsideration is respectfully solicited. The Examiner may address any questions raised by this submission to the undersigned at 617-951-7000. Should an extension of time be required, Applicants hereby petition for same and request that the extension fee and any other fee required for timely consideration of this submission be charged to **Deposit Account No. 18-1945**.

Date: July 5, 2001

Customer No: 28120
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Ropes & Gray
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Respectfully Submitted,



David P. Halstead
Reg. No. 44,735



results of BLAST

BLASTP 2.1.3 [Apr-11-2001]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 992903094-22877-12488

Query=

(339 letters)

Database: pat

71,783 sequences; 10,525,338 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 503 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments

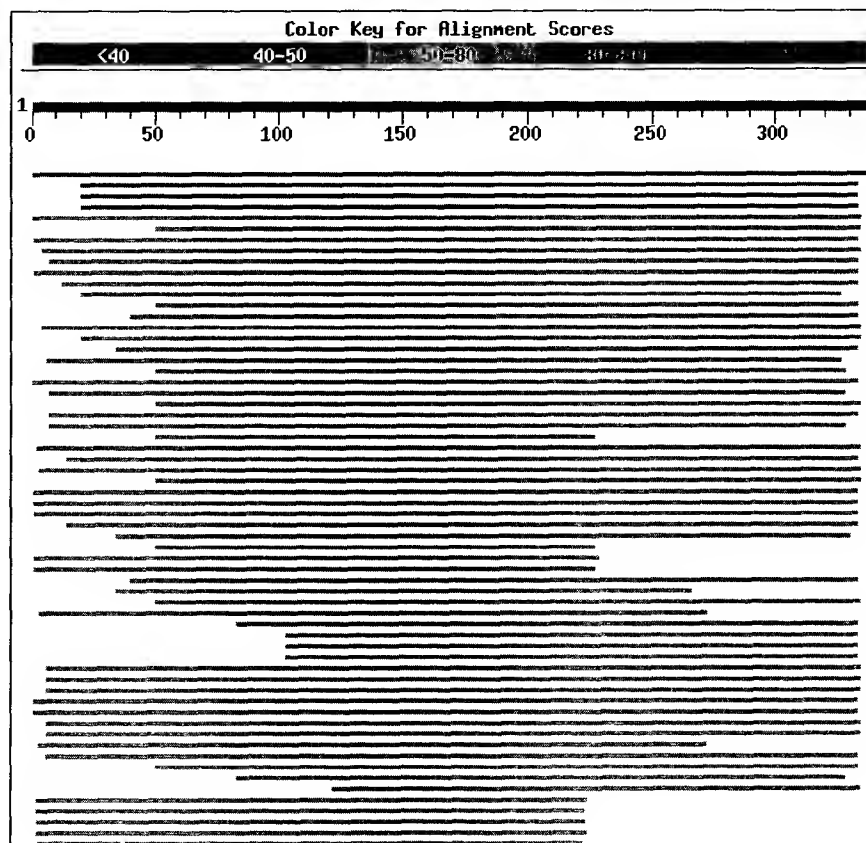


EXHIBIT A

Sequences producing significant alignments:				Score (bits)	E Value
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gi 6733419 emb CAB69315.1	(A84499) unnamed protein product...	82	4e-16		
gi 10061049 gb AAE37002.1	Sequence 2 from patent US 5986055	82	4e-16		
gi 6733417 emb CAB69314.1	(A84497) unnamed protein product...	82	4e-16		
gi 11340555 emb CAC17042.1	(AX040958) unnamed protein prod...	78	9e-15		
gi 12225900 emb CAC21767.1	(AX048754) unnamed protein prod...	76	4e-14		
gi 11340559 emb CAC17043.1	(AX040962) unnamed protein prod...	74	8e-14		
gi 10057862 gb AAE34768.1	Sequence 5 from patent US 5977442	74	8e-14		
gi 2491504 gb AAB79640.1	I64354 Sequence 2 from patent US 5...	74	1e-13		
gi 5950570 gb AAE04796.1	Sequence 2 from patent US 5869043	73	2e-13		
gi 10057864 gb AAE34770.1	Sequence 7 from patent US 5977442	72	5e-13		
gi 10057863 gb AAE34769.1	Sequence 6 from patent US 5977442	71	7e-13		
gi 4001196 gb AAC94628.1	AR025720 Sequence 20 from patent U...	71	7e-13		
gi 10057861 gb AAE34767.1	Sequence 4 from patent US 5977442	71	1e-12		
gi 11340563 emb CAC17044.1	(AX040966) unnamed protein prod...	70	2e-12		
gi 12827408 gb AAE50558.1	Sequence 17 from patent US 6114517	69	3e-12		
gi 1831632 gb AAB46086.1	Sequence 16 from patent US 559590...	69	3e-12		
gi 4001195 gb AAC94627.1	AR025719 Sequence 19 from patent U...	69	4e-12		
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gi 5955786 gb AAE07442.1	Sequence 9 from patent US 5801015	68	8e-12		
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gi 10058203 gb AAE35109.1	Sequence 2 from patent US 5981248	68	9e-12		
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gi 12225908 emb CAC21769.1	(AX048762) unnamed protein prod...	67	1e-11		
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gi 1831631 gb AAB46085.1	Sequence 15 from patent US 559590...	66	3e-11		
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gi 1831630 gb AAB46084.1	Sequence 14 from patent US 559590...	65	5e-11		
gi 10058204 gb AAE35110.1	Sequence 4 from patent US 5981248	65	5e-11		
gi 10049308 gb AAE26215.1	Sequence 2 from patent US 5948885	65	6e-11		
gi 5942087 gb AAE01619.1	Sequence 3 from patent US 5858765	65	6e-11		
gi 3997995 gb AAC91427.1	AR017537 Sequence 14 from patent U...	65	6e-11		
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gi 10051521 gb AAE28428.1	Sequence 31 from patent US 5958784	64	1e-10		
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gi 14100017 gb AAE53157.1	Sequence 46 from patent US 6140124	62	4e-10		
gi 2491505 gb AAB79641.1	I64355 Sequence 3 from patent US 5...	62	4e-10		
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gi 10057865 gb AAE34771.1	Sequence 8 from patent US 5977442	61	1e-09		
gi 1252508 gb AAA93767.1	Sequence 2 from patent US 5459036	61	1e-09		
gi 10067610 gb AAE40373.1	Sequence 8 from patent US 6001580	61	1e-09		
gi 10051520 gb AAE28427.1	Sequence 30 from patent US 5958784	61	1e-09		
gi 3012816 gb AAC11659.1	I76662 Sequence 43 from patent US ...	60	2e-09		

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gi 14103310 gb AAE54744.1	Sequence 2 from patent US 615341...	59	3e-09
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gi 3997604 gb AAC91034.1	AR017146 Sequence 6 from patent US...	58	8e-09
gi 1831629 gb AAB46083.1	Sequence 13 from patent US 559590...	58	8e-09
gi 12225932 emb CAC21775.1	(AX048786) unnamed protein prod...	58	9e-09
gi 12811293 gb AAE44306.1	Sequence 2 from patent US 6080557	58	1e-08
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gi 9998363 emb CAC07562.1	(AX012313) unnamed protein produ...	57	1e-08
gi 5951591 gb AAE05817.1	Sequence 38 from patent US 586964...	57	2e-08
gi 10057866 gb AAE34772.1	Sequence 9 from patent US 5977442	57	2e-08
gi 10067622 gb AAE40379.1	Sequence 14 from patent US 6001580	56	3e-08
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gi 1831628 gb AAB46082.1	Sequence 12 from patent US 559590...	56	3e-08
gi 6733345 emb CAB69292.1	(A84425) unnamed protein product...	56	3e-08
gi 1831623 gb AAB46077.1	Sequence 4 from patent US 5595904...	56	3e-08
gi 6733363 emb CAB69301.1	(A84443) unnamed protein product...	56	3e-08
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gi 10051515 gb AAE28422.1	Sequence 25 from patent US 5958784	54	1e-07
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gi 2830537 gb AAC00741.1	I68415 Sequence 30 from patent US ...	54	1e-07
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gi 12813500 gb AAE44800.1	Sequence 29 from patent US 6083713	54	2e-07
gi 10051526 gb AAE28433.1	Sequence 36 from patent US 5958784	53	2e-07
gi 10051513 gb AAE28420.1	Sequence 23 from patent US 5958784	53	3e-07
gi 2725137 gb AAB92819.1	I67157 Sequence 25 from patent US ...	53	3e-07
gi 5944578 gb AAE02654.1	Sequence 9 from patent US 5861300...	53	3e-07
gi 2489138 gb AAB77274.1	I57259 Sequence 11 from patent US ...	52	3e-07
gi 10043358 emb CAC07738.1	(AX019387) unnamed protein prod...	52	3e-07
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gi 12225920 emb CAC21772.1	(AX048774) unnamed protein prod...	52	6e-07

Alignments

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Score = 624 bits (1609), Expect = e-179
Identities = 333/339 (98%), Positives = 335/339 (98%)

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Sbjct: 1  MKLSDYYIDKELIYNSAISDIYTAIDKFNNLPVCLKIVDEDFSLPPHSIHREVLILKTLK 60

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Sbjct: 61  PHPNIIIEYFNDLKICDDIILVTKLYRYDLSQLIEITKYCKRTRTFIYGINGNLVSNQYTL 120

Query: 121 ANEIEEKDIKLWLKSMSSGLEFIHSQGIHRDIKPSNIFFARDDITQPIIGDFDICYDLK 180
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Query: 301 DIILPRCNDLDMKEIFTKMIRYDRSKRITSKEILQLMLD 339
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Identities = 82/316 (25%), Positives = 141/316 (43%), Gaps = 54/316 (17%)

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Query: 139 GLEFIHSQGIHRDIKPSNIFFARDDITQPIIGDFDICYDLKLPPKDEPPMAKYIDVSTG 198
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 Sbjct: 360 GLAFCHSHRVLHRDLKPQNLLINTEGAIK--LADFGGLARAFGVPVRTYTH-----EVVTL 412

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 IF GTP+ + +Y K + K+ R+D+ ++P ++D + + ++
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>gi|10061049|gb|AAE37002.1| Sequence 2 from patent US 5986055
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Score = 82.2 bits (202), Expect = 4e-16

Identities = 82/316 (25%), Positives = 141/316 (43%), Gaps = 54/316 (17%)

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 Sbjct: 18 VYKARNKLTGEVVALKKIRLDTETEGVPSTAIREISLLKELN-HPNIVKLLDVIHTENKL 76

Query: 79 ILVTKLYRYDLSQLIEITKYCKRTTRFIYGINGNLVSNQYTLANEIEEKDIKLWLKSMSS 138
 LV + DL + ++ + + GI L IK +L +
 Sbjct: 77 YLVFEFLHQDLKKFMDASA-----LTGIPLPL-----IKSYLFQLLQ 113

Query: 139 GLEFIHSQGIHRDIKPSNIFFARDDITQPIIGDFDICYDLKLPPKDEPPMAKYIDVSTG 198
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Query: 199 IYKAPELILGITNYEYEIDIWSLGIILTGLYSENFQSVLVKDDKELTNDSHVSDLYLLNQ 258